



SEQUENCE LISTING

<110> Sagami Chemical Research Center, Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661924

<140> US/10/019,151

<141> 2003-01-31

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met
1 5 10 15

Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly
20 25 30

Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr
35 40 45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
50 55 60

Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
65 70 75 80

Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
85 90 95

Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
100 105 110

Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
115 120 125

Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
130 135 140

Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160

Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175

Asn Arg Pro His Pro Trp Gly Leu Leu Thr Phe Ile Glu Leu Ile
180 185 190

Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
195 200 205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
210 215 220

Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
225 230 235

<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
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Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
20 25 30
Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
35 40 45
Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
50 55 60
Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80
Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85 90 95
Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110
Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125
Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140
Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160
Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175
Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205
Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210 215 220
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
260 265 270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
275 280 285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
290 295 300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
305 310 315 320
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
325 330 336
Arg Arg Arg

<210> 3

<211> 326

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu
1 5 10 15
Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser
20 25 30
Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro
35 40 45
Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser
50 55 60
Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

65	70	75	80
Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly			
85	90	95	
Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys			
100	105	110	
Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp			
115	120	125	
Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser			
130	135	140	
Phe Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys			
145	150	155	160
Gly Leu Lys Leu Ser Ala Ala Val Ser Ser Val Leu Ser Gly			
165	170	175	
Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala			
180	185	190	
Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr			
195	200	205	
Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala			
210	215	220	
Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe			
225	230	235	240
Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro			
245	250	255	
His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr			
260	265	270	
Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His			
275	280	285	
Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly			
290	295	300	
Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser			
305	310	315	320
Val Glu Glu Glu Gln Cys			
	325		

<210> 4
<211> 324
<212> PRT
<213> Homo sapiens

<400> 4	1	5	10	15
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Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg				
20	25	30		
Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala				
35	40	45		
Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu				
50	55	60		
Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr				
65	70	75	80	
Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala				
85	90	95		
Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys				
100	105	110		
Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr				
115	120	125		
Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser				
130	135	140		
Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr				
145	150	155	160	

Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
165 170 175
Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
180 185 190
Val Gln Ala Glu Leu Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys
195 200 205
Leu Leu Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val
210 215 220
Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala
225 230 235 240
Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr
245 250 255
Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly
260 265 270
Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly
275 280 285
Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly
290 295 300
Gly Ile Val Phe Leu Ala Phe Ser Ala Leu Phe Ile Ser Pro
305 310 315 320
Asp Ser Gly Phe

<210> 5
<211> 153
<212> PRT
<213> Homo sapiens

<400> 5
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
1 5 10 15
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
20 25 30
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
35 40 45
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
50 55 60
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
65 70 75 80
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr
85 90 95
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu
100 105 110
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr
115 120 125
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly
130 135 140
Val Arg Ile Phe Gly Ile Asn Lys Tyr
145 150

<210> 6
<211> 153
<212> PRT
<213> Homo sapiens

<400> 6
Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
1 5 10 15
Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu
20 25 30
Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val

35	40	45	
Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu			
50	55	60	
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala			
65	70	75	80
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr			
85	90	95	
Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu			
100	105	110	
Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr			
115	120	125	
Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly			
130	135	140	
Val Arg Val Phe Gly Ile Asn Lys Tyr			
145	150		

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala			
1	5	10	15
Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp			
20	25	30	
Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe			
35	40	45	
Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg			
50	55	60	
Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu			
65	70	75	80
Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val			
85	90	95	
Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe			
100	105	110	
Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser			
115	120	125	
Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val			
130	135	140	
Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys			
145	150	155	160
Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met			
165	170	175	
Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr			
180	185	190	
Leu Glu Lys Thr Ile His Glu Glu			
195	200		

<210> 8

<211> 189

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Gly Ala Trp Ala			
1	5	10	15
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro			
20	25	30	
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu			

35	40	45
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu		
50	55	60
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg		
65	70	75
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser		
85	90	95
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg		
100	105	110
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val		
115	120	125
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu		
130	135	140
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln		
145	150	155
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly		
165	170	175
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu		
180	185	

<210> 9
<211> 714
<212> DNA
<213> Homo sapiens

<400> 9

atgattctgc ttgtgattct tgcattttat ctgtggcagg tggacatgtt gagtcaaattt	60
aacattgttc cccggattct caccaatttc actggagtaa tgccacactca gttcaaaaag	120
gattttggatt cctatcttaa aactcgatca ccagtcaactt tcctgtctga tctgcgcagc	180
aacctacagg tatccaatga acctggaaat cgctacaacc tccagctcat caatgcactg	240
gtgctctatg tcgggactca ggccattgcg cacatccaca acaagggcag cacacccatca	300
atgagcacca tcaactcactc agcacacatg gatatctcc agaatttggc tgtggacttg	360
gacactgagg gtcgctatct ctttttgaat gcaattgcaa atcagctccg gtacccaaat	420
agccacacact actactttag ttgacccatg ctgtacccctt ttgcagaggc caatacggaa	480
gccatccaag aacagatcac aagagttctc ttggAACGGT tgattgtaaa taggcacat	540
cttgggggtc ttcttattac cttcatttag gtcattaaaa acccagcggt taagttctgg	600
aaccatgaat ttgtacactg tgccccagaa atcgaaaatg tattccagtc ggtcgacacag	660
tgctgcatgg gacagaagca ggcccagcaa gtaatggaa ggacaggtgc cagt	714

<210> 10
<211> 1017
<212> DNA
<213> Homo sapiens

<400> 10

atggccgcag cctgcgggccc gggagcggccc gggtaactgct tgccctcggtt cttgcatttg	60
tttctgtca cccggggccc tgcctggcc tggAACGACC ctgacagaat gttgtcgcc	120
gatgtaaaag ctcttaccct ccactatgac cgctataccca cctcccgccag gctggatccc	180
atcccacagt tgaaaatgtgt tggaggcaca gctgggttgtg attcttatac cccaaaagtc	240
atacaatgttc agaacaaaagg ctggatggg tatgatgtac agtggaaatg taagacggac	300
ttagatatttgc catacaaaattt tggaaaaactt gtggtagact gtgaaggcta tgagtccct	360
gaagaccagt atgtactaag aggttcttgcg ggcttggagt ataattttaga ttatacagaa	420
cttggcctgc agaaaactgaa ggagtcgtt aagcagcacg gcttgcctc tttctctgtat	480
tattattata agtggtcctc ggcgattcc tgcataatgtat gtggattgtat taccatcgat	540
gtactccttg ggatcgccctt tgcataatgtat aagctgttcc tgagtgcgg gcagtttct	600
cctccaccgt actctgtatca tcctccattt tcccaccgtt accagagatc caccacactca	660
gcaggacctc ctccccccagg cttaaagtctt gagttcacag gaccacagaa tactggccat	720
ggtgcaactt ctggttttgg cagtgcctt acaggacac aaggatatgtaa aattcagga	780
ccagggttctt ggacaggctt gggactgtt ggaataacttag gatattgtt tggcagcaat	840
agagcggcaa cacccttctc agactcgatgg tactaccgtt cctatcctcc ctcctaccct	900

ggcacgtgga atagggctta ctcacccctt catggaggct cgggcagcta ttcggtatgt 960
tcaaactcag acacgaaaac cagaactgca tcaggatatg gtggtaccag gagacga 1017

<210> 11
<211> 978

<212> DNA

<213> Homo sapiens

<400> 11

atggccaaga tggagcttc gaaggccttc tctggccagc ggacactcct atctgccatc 60
ctcagcatgc tatcactcag ctctccaca acatccctgc tcagcaacta ctggtttg 120
ggcacacaga aggtggccaa gcccctgtgc gagaaaggc tggcagccaa gtgcttgac 180
atgccagtgt ccctggatgg agataccaac acatccaccc aggaggttgt acaataaac 240
tgggagactg gggatgacgg gttctcctc cggagcttc ggagtggcat gtggctatcc 300
tgtgaggaaat ctgttggaaa accaggggag aggtggccaa gtttcattga acttacacca 360
ccagccaaga gagaatctt atggttatcc ctgggaacgc agatcaccta catcgactt 420
caattcatca gcttccctc gctactaaca gacttgcac tcactggaa ccctgcctgt 480
gggctcaaacc tgagcgcctt tgctgctgtt tcctctgtcc tgtaggtct cctgggatg 540
gtggcccaaca tgatgttattc acaagtcttc caagcgactg tcaacttggg tccagaagac 600
tggagaccac atgtttggaa ttatggctgg gccttctaca tggcctggct ctcttcacc 660
tgctgcatgg cgtcggtgtt caccaccc aacacgtaca ccaggatgtt gctggagttc 720
aagtgcagaat atagaaggat ttcaaggaa aacccgaaac gcctaccaca tcaccatcag 780
tgttccctc ggcggctgtc aagtgcagcc cccaccgtgg gtccttgcac cagctaccac 840
cagtatcata atcagcccat ccactctgtc tctgaggggag tcgacttcta ctccgagctg 900
cggaacaagg gatttcaagg agggggcagc caggagctga aagaagcagt taggtcatct 960
gtagaggaag agcagtgt 978

<210> 12

<211> 972

<212> DNA

<213> Homo sapiens

<400> 12

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ctgggtccgc tgctgtggc cccggctgcg gtccggggcg gcccagatga agaccttagc 120
caccggaaaca aagaaccggc ggcggccggcc cagcagctgc agccgcagcc tggctgt 180
caggggccccg agccggcccg ggtcgagaaa atatttacac cagcagctcc agttcatacc 240
aataaagaag atccctgctac ccaaactaat ttgggattta tccatgcatt tgctgctg 300
atatcagttt ttattgttata tgaattgggt gataagacat ttttatagc agccatcatg 360
gcaatgcgtt ataaccgcctt gaccgtgtt gctgggtcctt tgcttgcctt gggactaatg 420
acatgcttgtt cagttttttt tggctatgccc accacagtca tcccccagggtt ctatacatac 480
tatgtttcaa ctgttatttt tgccatttt ggcattagaa tgcttcggga aggcttaaag 540
atgagccctg atgagggtca agagaactg gaagaagttc aagctgaatt aaagaagaaaa 600
gatgaagaat ttcaacgaac caaactttt aatggaccgg gagatgttga aacgggtaca 660

agcataacac tacctcagaa aaagtgggtt catttttattt cacccatttt tggtaagct 720

cttacattaa cattcttagc agaatgggtt gatcgcttc aactaactac aattgtattt 780

gcagcttagag aggaccccta tgggttagcc gtgggtggaa ctgtggggca ctgcctgtgc 840

acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg 900

acaatcatag gaggcatgtt tttttggcg tttgcatttt ctgcactatt tataagccct 960
gattctgggtt tt 972

<210> 13

<211> 459

<212> DNA

<213> Homo sapiens

<400> 13

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ggcatctggc	tctcctacgt	gctgccatc	ggtctccctc	acatcgtgt	gctgaggatc	120
ccgttgtga	gtgtccctgt	cgtctggacc	ctcaccaacc	tcattcacaa	catgggcatg	180
tatatcttcc	tgcacacgt	gaaggggaca	ccctttgaga	ccccggacca	gggcaaggcg	240
aggctgctaa	cccactggg	gcagatggat	tatggggtcc	agttcacggc	ctctcgaaag	300
ttcttgacca	tcacacccat	cgtgctgtac	ttcctcacca	gcttctacac	taagtacgac	360
cagatccatt	ttgtgctcaa	caccgtgtcc	ctgatgagcg	tgcttatccc	caagctgccc	420
cagctccacg	gagtccggat	tttttggaaatc	aataagtac			459

<210> 14

<211> 459

<212> DNA

<213> Homo sapiens

<400> 14

atgaatgtgg	gggtggcaca	cagcgaagta	aaccccaaca	cccggagtat	gaatagccga	60
ggcatctggc	ggcctacat	catcttggta	ggattgctgc	atatggttct	actcagacatc	120
cccttcttca	gcattctgt	tgtctggacc	ctgacccaac	tcatccataa	cctggctacg	180
tatgtcttcc	ttcatacgt	gaaagggaca	ccctttgaga	ctcctgacca	aggaaaggct	240
cggctactga	cacactggg	gcaaatggac	tatgggcctc	agtttacctc	ttcccgcgaag	300
ttcctcagca	tctctcttat	tgtgctctat	ctcctggcca	gcttctatac	caagtatgat	360
gctgcccact	tcctcatcaa	cacagccta	ttgctaagt	tactgctgcc	gaagttgccc	420
cagttccatg	gggttcgtgt	ctttggcatc	aacaaataac			459

<210> 15

<211> 600

<212> DNA

<213> Homo sapiens

<400> 15

atggcagcat	ctatgcatgg	tcagcccaat	ccttctctag	aagatgaaaa	actcagaaga	60
ccaatggtca	tagaaatcat	agaaaaaaat	tttgactatc	tttagaaaaga	aatgacacaaa	120
aatatatatc	aatggcgac	atttggaaaa	acagctgttt	tctctggaat	attctcaaac	180
ttcctgttca	gacgctgttt	caaggtaaa	catgtgttt	tgaagacata	tgcatttttg	240
gctacacttc	cattttttgtc	tactgtgtt	actgacaagc	tttttgtat	tgtgtcttg	300
tattcagata	atataagcaa	ggaaaactgt	tttttcagaa	gctcaactgt	tggcatagtt	360
tgtgggttt	tctatcccag	ttcttggct	tttactaaaa	atgacgcct	ggcaacccaag	420
tatcataccg	ttccactgca	accaaaaagg	agggtttaa	tccattggat	gacgctttgt	480
caaacacaaa	tgaaattaa	ggcgattct	ctagtcttc	agattatgtt	tggaaatatta	540
aatggcttat	accattatgc	agtatttggaa	gagacacttg	agaaaactat	acatgaagag	600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

atgaggctgt	cactgccact	gctgctgt	ctgctggag	cctggccat	cccagggggc	60
ctcgccgaca	gggcgccact	cacagccaca	gccccacaa	tggatgtat	ggagatgtac	120
tcagcccaca	tgccccctca	cctgcgtgt	gatgcgtca	gagctgtggc	ttaccagatg	180
tggcaaaatc	tggcaaaggc	agagacaaa	tttcataacct	caaactctgg	ggggcggcgg	240
gagctgagcg	agttggtcta	cacgatgtc	ctggaccgga	gctgctccc	gaactggcag	300
gactacggag	tgcgagaagt	ggaccaagt	aaacgtctca	cagggccagg	acttagcgag	360
ggccagagc	caagcatca	cgtgatggc	acagggggcc	cctggctac	caggctctcc	420
aggacatgtt	tgcactactt	gggggagttt	ggagaagacc	agatctatga	agcccaccaa	480
caagggccgag	gggctctgga	ggcattgtat	tgtggggac	cccagggggc	ctgctcagag	540
aagggtgtcag	ccacaagaga	agagctc				567

<210> 17
<211> 1167
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (187) ... (903)

<400> 17
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ttcttcataa gaaagaaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120
tatagtgtat atagtttag aaaaacagtc ccaccactta agcatagatg taatttacta 180
ataaaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228
Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val
1 5 10
gac atg ttg agt gaa att aac att gct ccc cggtt att ctc acc aat ttc 276
Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe
15 20 25 30
act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324
Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu
35 40 45
aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372
Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu
50 55 60
cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420
Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn
65 70 75
gca ctg gtg ctc tat gtc ggg act cag gcc att gct cac atc cac aac 468
Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn
80 85 90
aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516
Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met
95 100 105 110
gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat 564
Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr
115 120 125
ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac 612
Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His
130 135 140
act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat 660
Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn
145 150 155
acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg 708
Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Glu Arg Leu
160 165 170
att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag 756
Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu
175 180 185 190
ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac 804
Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His
195 200 205
tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc 852
Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys
210 215 220
atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900
Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser
225 230 235
tagacgaaac tgcatctcg ttgtacgtt cagtctagag gtctcaactgc accgagttca 960
taaactgact gaagaatcct ttcagcttt cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactgtt gggatcagcc tcctgtctta tggggcacg ttccaaagtt 1080
taaatgcatt ttttgactc ttggccaaaa tttagaagat gctgtgaata tcatttgaa 1140
cttgtgtaaa tacatgaaag agaaaac 1167

<210> 18
<211> 1925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (115) ... (1134)

<400> 18
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cccaggttcg gccccgtggc gtctggcagc ccggcccat cttcatcgag cgcc atg 117
Met
1
gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Gly
5 10 15
ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
20 25 30
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
35 40 45
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
Asp Arg Tyr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
50 55 60 65
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
Cys Val Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
70 75 80
cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
85 90 95
aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
100 105 110
tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
115 120 125
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
130 135 140 145
ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
150 155 160
tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
165 170 175
acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
180 185 190
ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
195 200 205
ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
210 215 220 225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt	837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly	
230 235 240	
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa	885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu	
245 250 255	
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta	933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Ile Leu	
260 265 270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg	981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser	
275 280 285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg	1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg	
290 295 300 305	
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca	1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser	
310 315 320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg	1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg	
325 330 335	
aga cga taaagttagaa agttggagtc aaacactgga tgcagaaaatt ttggatttt	1180
Arg Arg	

tcatcacttt ctcttttagaa aaaaagtact acctgttaac aattggaaaa agggatatt	1240
caaaagttct gtgggtttat gtccagtgtat gctttttgtat ttcttatttt tgaggctaaa	1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgttatatt	1360
gcagtttttg aaagtgtatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct	1420
gtgatgccct aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa	1480
aatttcagtt ttaggtgggtt gtagctgatg agttattacc tcatagagac tataatattc	1540
tatttgttat tatattttt gatgtttgtt gttcttcaaa catttaaattc aagctttgga	1600
ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca	1660
gtgggtggaga tggccttcgt gtaactgaat attacctct gttagaaaaag gtggaaaaata	1720
agcatctaga aggttgggtt gaatgactct gtgctggcaa aaatgcttga aacctctata	1780
tttcttcgt tcataagagg taaaggtcaa attttcaac aaaagtcttt taataacaaa	1840
agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgttc aatctaaaaa	1900
agaatcaata aaaacaaaca aggggg	1925

<210> 19
<211> 1125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (71)...(1051)

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Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln	
1 5 10	
cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc	157
Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser	
15 20 25	
aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg	205
I]Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val	
30 35 40 45	
ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg	253
Pro Lys Pro Leu Cys Glu Lys Ala Ala Lys Cys Phe Asp Met	

50	55	60	
cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag	gtg gta		301
Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val			
65	70	75	
caa tac aac tgg gag act ggg gat gac cggttc tcc ttc cgg agc ttc			349
Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe			
80	85	90	
cggttgttgcata tcc ttttgc gaa act gtg gaa gaa cca ggg			397
Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly			
95	100	105	
gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa			445
Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu			
110	115	120	125
atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa			493
Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln			
130	135	140	
ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac			541
Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn			
145	150	155	
cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc			589
Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val			
160	165	170	
ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc			637
Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val			
175	180	185	
ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt			685
Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val			
190	195	200	205
tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc			733
Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys			
210	215	220	
tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg			781
Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val			
225	230	235	
ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac			829
Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn			
240	245	250	
tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca			877
Cys Leu Pro His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala			
255	260	265	
gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag			925
Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln			
270	275	280	285
ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg			973
Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg			
290	295	300	
aac aag gga ttt caa aag ggg gcc agc cag gag ctg aaa gaa gca gtt			1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val			
305	310	315	
agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggttgg gg			1070
Arg Ser Ser Val Glu Glu Gln Cys			
320	325		
agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc			1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> (40) ... (1014)

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 Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Phe Leu 1 5
 10 15 20
 ccg gag aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102
 Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Phe Leu
 Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu 25 30 35
 150
 gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg 198
 Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu
 40 45 50
 246
 cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu 55 60 65
 Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro 294
 70 75 80 85
 342
 gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile 90 95 100
 tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca 390
 Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala 105 110 115
 438
 gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala 120 125 130
 486
 atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr 135 140 145
 534
 gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val 150 155 160 165
 582
 tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met 170 175 180
 630
 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Val Gln Ala Glu Leu 185 190 195
 678
 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro 200 205 210
 726
 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp 215 220 225
 774
 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe 230 235 240 245
 822
 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala 250 255 260
 870
 gct aga gag gac ccc tat ggt gta gcc gtc ggt gga act gtg ggg cac Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His 265 270 275
 918
 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln

280	285	290	
aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg			966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu			
295	300	305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt			1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe			
310	315	320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat			1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat ttgttagcac tgattttgtg			1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatgttaaa caaggagttt			1190
taaaagaaac ctgacttcta agtgtgggtt ttcttctct ccaacataat tatgttaata			1250
tggtcctcat ttcttcttgc gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt			1310
ctttcagcac tgacccctt ttaaggaata caaatttct cttcatcac ttaggtgttt			1370
taagatgttt accttaaagt ttcttcttggg gaaagaatga attaatttct atttcttaaa			1430
acatttccc gagccagtaa acagtagttt aatcatttgtt ctttcaaaa ctaggtgttt			1490
aaaaaaaaagag acatataatga tattgctgtt atatcaataa catggcacaa caagaactgt			1550
ctgccaggc attcttcctc ttttttttt aattgggttag gacacccaat ataaaaaacag			1610
tcaatatttgc acaatgtgga attaccaaataa taaaagagaa tactatgaat gtattcatat			1670
ttttctata ttgaataaac aatgtAACat agataacaataaataaaaaa gtggtatgac			1730
cagt			1734

<210> 21
<211> 2064
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (98)...(559)

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cttcggcccc acacgaacag cagaggggg cagcagg atg aat gtg ggc aca			112
Met Asn Val Gly Thr			
1	5		
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc			160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly			
10	15	20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg			208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu			
25	30	35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac			256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn			
40	45	50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg			304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly			
55	60	65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac			352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His			
70	75	80	85
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cggt aag ttc			400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe			
90	95	100	
ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act			448
Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr			
105	110	115	
aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc			496
Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser			
120	125	130	
gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cggtt att ttt gga			544

<210> 22
<211> 570
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (28) . . . (489)

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<400> 22
agccggacgg gatatctgagc tggcagg atg aat gtg ggg gtg gca cac agc      51
                           Met Asn Val Gly Val Ala His Ser
                           1           5
gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg      99
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu
   10          15          20
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc     147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile
   25          30          35          40
ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat     195
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His
   45          50          55
aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt     243

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Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe			
60	65	70	
gag act cct gac caa gga aag gct cggtt cta ctg aca cac tgg gag caa		291	
Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln			
75	80	85	
atg gac tat ggg ctc cag ttt acc tct tcc cgcc aag ttc ctc agc atc		339	
Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile			
90	95	100	
tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat		387	
Ser Pro Ile Val Leu Tyr Leu Ala Ser Phe Tyr Thr Lys Tyr Asp			
105	110	115	120
gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg		435	
Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu			
125	130	135	
ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa		483	
Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys			
140	145	150	
tac tgag ggatgggttt tgggacagct ccatgggcat ggggaaggca ctgaaacaga		540	
Tyr			
ggactataaa acatccttct cttattctcc		570	
<210> 23			
<211> 1161			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (278) ... (880)			
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ggtgttgtc cgggtggaaac tgaggaagcg cccaaaggaaa tgaaacacga tttccaaat		120	
gaacttaatc tttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca		180	
cctccccacc tgaagagcta ggaggacaac tacaaagagc ctgactgcct tctcgaaatg		240	
aggagagagg aaaacagcaa cagtatcgt tttcaag atg gca gca tct atg		292	
Met Ala Ala Ser Met			
1	5		
cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca		340	
His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro			
10	15	20	
atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa		388	
Met Val Ile Glu Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu			
25	30	35	
atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt		436	
Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly			
40	45	50	
ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt		484	
Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val			
55	60	65	
aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt		532	
Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe			
70	75	80	85
ttg tct act gtt act gac aag ctt ttt gta att gat gct ttg tat		580	
Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr			
90	95	100	
tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att		628	
Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile			
105	110	115	

ggc ata gtt tgt ggt ttc tat ccc agt tct ttg gct ttt act aaa	676
Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys	
120 125 130	
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa	724
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys	
135 140 145	
gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa	772
Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys	
150 155 160 165	
tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat	820
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn	
170 175 180	
ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata	868
Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile	
185 190 195	
cat gaa gag taacccaaaa aatgaatgg tgctaactta gcaaatgaa gtt	920
His Glu Glu	
200	
tctataaaga ggactcagggc attgctgaaa gagttaaaag taactgtgaa caaataattt	980
gttctgtgcc ttttgccctgg tatatacgaa atactcaaaa agtattcaat aattcaatca	1040
ataaatataa gtttcatctt acacgtaaga tacaggtctt atccctgat ggtgtgtcca	1100
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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Gly Ala Trp Ala	
1 5 10 15	
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca	153
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro	
20 25 30	
caa ctg gat gag gag atg tac tca gcc cac atg ccc gct cac ctg	201
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu	
35 40 45	
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg	249
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu	
50 55 60	
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg	297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg	
65 70 75 80	
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc	345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser	
85 90 95	
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt	393
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg	
100 105 110	
ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg	441
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val	

115	120	125	
atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg			489
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu			
130	135	140	
cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa			537
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln			
145	150	155	160
caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg			585
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly			
165	170	175	
gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc			630
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu			
180	185		
tggactctac cctcctctga aagaagctgg ggcttgctct gacggctctcc actcccgct			690
gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccattctgccc tccctctcc			750
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